

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 16:41:42 ; Search time 54.4414 Seconds
(without alignments)
1362.510 Million cell updates/sec

Title: US-09-625-573-4

Perfect score: 1900

Sequence: 1 MISTRSRFRINTNESGEV.....DGVSTNTSTGQEVSAAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mnc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_undefined.*
- 15: sp_rvirus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1392 | 73.3 | 352 | 6 Q95NC2 | Q95nc2 calliobus |
| 2 | 1375 | 72.4 | 352 | 6 Q97776 | Q97776 cercopithec |
| 3 | 1375 | 72.4 | 352 | 6 Q9MZA0 | Q9mza0 callithrix |
| 4 | 1373 | 72.3 | 352 | 6 Q95NE1 | Q95ne1 cercopithec |
| 5 | 1371 | 72.2 | 352 | 6 Q9XT12 | Q9xtl2 cercopithec |
| 6 | 1371 | 72.2 | 352 | 6 Q95NC9 | Q95nc9 alouatta se |
| 7 | 1371 | 72.2 | 352 | 6 Q95NC4 | Q95nc4 ateles geof |
| 8 | 1368 | 72.0 | 352 | 6 Q18770 | Q18770 pan troglod |
| 9 | 1368 | 72.0 | 352 | 6 Q9TV49 | Q9tv49 cercopithec |
| 10 | 1367 | 71.9 | 352 | 6 Q9M299 | Q9m299 ateles sp. |
| 11 | 1366 | 71.9 | 352 | 6 Q95ND1 | Q95nd1 mandrillus |
| 12 | 1366 | 71.9 | 352 | 6 Q95NC0 | Q95nc0 hylobates m |
| 13 | 1365 | 71.8 | 352 | 6 Q9XS99 | Q9xs99 gorilla gor |
| 14 | 1365 | 71.8 | 352 | 6 Q95NC5 | Q95nc5 hylobates s |
| 15 | 1364 | 71.8 | 352 | 6 Q95ND2 | Q95nd2 mandrillus |
| 16 | 1364 | 71.8 | 352 | 6 Q95ND0 | Q95nd0 erythrocebu |

| | | | | | |
|----|------|------|-----|----------|--------------------|
| 17 | 1364 | 71.8 | 352 | 6 Q95NC1 | Q95nc1 theropithec |
| 18 | 1364 | 71.8 | 352 | 6 Q97975 | Q97975 macaca arct |
| 19 | 1363 | 71.7 | 352 | 6 Q9TV50 | Q9tv50 pan troglod |
| 20 | 1363 | 71.7 | 352 | 6 Q9TV93 | Q9tv93 macaca arct |
| 21 | 1362 | 71.7 | 352 | 6 Q95NC8 | Q95nc8 colobus pol |
| 22 | 1361 | 71.6 | 352 | 6 Q9XT13 | Q9xtl3 papio anubi |
| 23 | 1361 | 71.6 | 352 | 6 Q95NC7 | Q95nc7 nasalis lar |
| 24 | 1360 | 71.6 | 352 | 6 Q9TSK1 | Q9tsk1 cercopithec |
| 25 | 1360 | 71.6 | 352 | 6 Q9TV42 | Q9tv42 cercopithec |
| 26 | 1360 | 71.6 | 352 | 6 Q97962 | Q97962 pygathrix a |
| 27 | 1360 | 71.6 | 352 | 6 Q9XS35 | Q9xs35 macaca neme |
| 28 | 1359 | 71.5 | 352 | 6 Q9TV48 | Q9tv48 cercopithec |
| 29 | 1358 | 71.5 | 352 | 6 Q18771 | Q18771 pan troglod |
| 30 | 1358 | 71.5 | 352 | 6 Q18772 | Q18772 pan troglod |
| 31 | 1358 | 71.5 | 352 | 6 Q9XT14 | Q9xtl4 colobus gue |
| 32 | 1358 | 71.5 | 352 | 6 Q95NC3 | Q95nc3 miopithecus |
| 33 | 1357 | 71.4 | 339 | 6 Q9TV48 | Q9tv48 saguinus sp |
| 34 | 1357 | 71.4 | 352 | 6 Q9TV46 | Q9tv46 cercopithec |
| 35 | 1357 | 71.4 | 352 | 6 Q95NE8 | Q95ne8 cercopithec |
| 36 | 1357 | 71.4 | 352 | 6 Q9XT76 | Q9xt76 cercopithec |
| 37 | 1356 | 71.4 | 352 | 6 Q9TV44 | Q9tv44 cercopithec |
| 38 | 1355 | 71.3 | 352 | 6 Q9BGN5 | Q9bgn5 cercopithec |
| 39 | 1354 | 71.3 | 352 | 6 Q9MZA3 | Q9mza3 hylobates a |
| 40 | 1353 | 71.2 | 339 | 6 Q9TSN3 | Q9tsn3 macaca fasc |
| 41 | 1353 | 71.2 | 339 | 6 Q9TQT3 | Q9tqt3 callithrix |
| 42 | 1353 | 71.2 | 352 | 6 Q95NC6 | Q95nc6 trachypithe |
| 43 | 1352 | 71.2 | 352 | 6 Q9TV47 | Q9tv47 cercopithec |
| 44 | 1351 | 71.1 | 339 | 6 Q9TVU2 | Q9tvu2 alouatta ca |
| 45 | 1351 | 71.1 | 352 | 6 Q9TQX0 | Q9tqx0 cercopithec |

ALIGNMENTS

RESULT 1

Q95NC2 PRELIMINARY; PRT; 352 AA.

AC Q95NC2;
01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Calliobus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Calliobinae;
OC Calliobus.
OX NCBI_TaxID=9523;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177887; AAK43370.1;
DR InterPro; IPR000923; BlueCu1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 73.3%; Score 1392; DB 6; Length 352;
Best Local Similarity 75.4%; Pred. No. 6.7e-112;
Matches 263; Conservative 30; Mismatches 50; Indels 6; Gaps 2;

QY 18 EEVTFDDYDYG--PCHKFDVKOIGAQLLPPLYSLVFIFGVGNMLVLLINCKKLKC 75

Db 4 EVSPFIYDIDIGASEPCQKIDKQWGAQLLPPLYSMLVFLFGVGNMLVLLINCKRLKS 63

QY 76 LTDIYLLNLAISSLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFILLT 135

```

Db 64 MTDHYLLNLALSDLEFLFVFWAHYAAGQWDFGNTMCOFLTGLYFIFGFSGFIILLT 123
QY 136 IDRLAIYHVAFAKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVVCGPYP 195
Db 124 IDRLAIYHVAFAKARTVTFGVTSVITWVAVFASLFGIIFTRSQEGYHTCSPHFP 183
QY 196 RG----WNNFHTIMRNILGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIV 251
Db 184 FGQYRFWKNLETLKMWILGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIV 243
QY 252 YELFWTPYNIIVILLTFQEFFGLSNCESTSOLDQATQVTTETLGMTCCNPIIYAVGEX 311
Db 244 YELFWAPYNIIVILLTFQEFFGLSNCSNRLDQAMQVTTETLGMTCCNPIIYAVGEX 303
QY 312 FRYLSVFRKHITRKQCKQCPVFEYRETVDGVTSTNTSTPSTGQEVSA 360
Db 304 FRYLLVFFQKHIAKFKCKCSIFQKEAPERANSVYTRSTGQEISVGL 352

RESULT 2
ID 07776 PRELIMINARY; PRT; 352 AA.
AC 07776;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chemokine receptor CCR5.
GN CCR5.
OS Cercopithecus torquatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciinae; Cercopithecinae.
OX NCBI_TaxID=81944;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1208;
RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
RA Aguilar R., Ho D.D., Marx P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
RT with a R2b-tropic simian immunodeficiency virus.";
RL J. Exp. Med. 0:0-0(1998).
DR EMBL; AF084004; AAC62472.1; -
DR InterPro; IPR0000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473D1D3 CRC64;

Query Match 72.4%; Score 1375; DB 6; Length 352;
Best Local Similarity 76.1%; Pred. No. 1.9e-110;
Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

QY 24 FDYDYG--GAPCHKFDVKQIGAGLLPPLYSLSVIFGFGVGNMVLVILINCKKLCRLDIYL 81
Db 10 YDIDYSEPCRKIDVKOMGAHLPLPLYSLSVIFGFGVGNMVLVILINCKKLSMTDIYL 69
QY 82 LNLALSLLFLTLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFILLTIDRYLA 141
Db 70 LNLALSLLFLTLVFWAHYAAGQWDFGNTMCOFLTGLYFIFGFSGFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVVVCGPYP----RG 197
Db 130 IVHAFALKARTVTFGVVTSVITWVAVFASLFGIIFTRSQEGYHTCSPHFPYQYOF 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFWT 257
Db 190 WNNFHTIMRNILGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFWA 249
QY 258 PYNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTCCNPIIYAVGEXKFRYLS 317
Db 250 PYNIVILLNTFOEFFGLSNCSNRLDQAMQVTTETLGMTCCNPIIYAVGEXKFRNYLA 309

```

```

Db 250 PYNIVILLNTFOEFFGLSNCSNRLDQAMQVTTETLGMTCCNPIIYAVGEXKFRNYLL 309
QY 318 VFFRKHITRKQCKQCPVFEYRETVDGVTSTNTSTPSTGQEVSA 360
Db 310 VFFOKHIAKFKCKCSIFQKEASERASSVYTRSTGQEISVGL 352

RESULT 3
ID 09MZA0 PRELIMINARY; PRT; 352 AA.
AC 09MZA0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CC chemokine receptor 5 (C-C chemokine receptor 5).
GN CCR5.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317091; PubMed=10747879;
RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA Begum K., Galvis M.C., Kostecky V., Valente A.J., Murchy K.K.,
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
RT and mRNA. Potential roles for haplotype and mRNA diversity,
RT differential haplotype-specific transcriptional activity, and altered
RT transcription factor binding to polymorphic nucleotides in the
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF252554; AAF87984.1; -
DR EMBL; AF177878; AAK43361.1; -
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;

Query Match 72.4%; Score 1375; DB 6; Length 352;
Best Local Similarity 75.2%; Pred. No. 1.9e-110;
Matches 258; Conservative 33; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDYG--APCHKFDVKQIGAGLLPPLYSLSVIFGFGVGNMVLVILINCKKLCRLDIYL 81
Db 10 YDIDYSEPCRKIDVKOMGAHLPLPLYSLSVIFGFGVGNMVLVILINCKKLSMTDIYL 69
QY 82 LNLALSLLFLTLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFILLTIDRYLA 141
Db 70 LNLALSLLFLTLVFWAHYAAGQWDFGNTMCOFLTGLYFIFGFSGFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVVVCGPYP----RG 197
Db 130 IVHAFALKARTVTFGVVTSVITWVAVFASLFGIIFTRSQEGYHTCSPHFPYQYOF 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFWT 257
Db 190 WNNFHTIMRNILGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFWA 249
QY 258 PYNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTCCNPIIYAVGEXKFRYLS 317
Db 250 PYNIVILLNTFOEFFGLSNCSNRLDQAMQVTTETLGMTCCNPIIYAVGEXKFRNYLA 309

```



```

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40420 MW; 3DBB43D1CCA48687 CRC64;

Query Match
Best Local Similarity 72.2%; Score 1371; DB 6; Length 352;
Matches 258; Conservative 30; Mismatches 49; Indels 6; Gaps 2;

QY 24 FDYDGA--PCHKFDVKQIGAOQLPPLYSLVFIFGVGNMVLVLLINCKKLCITDIYL 81
DB 10 YDIDYGASEPCQKTDVQKGAHLLPPLYSIVLFGVGNMVLVLLINCKRPSMTDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHGYFGGIFFIILLTIDRYLA 141
DB 70 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
DB 130 IVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFPGQYQF 189
QY 198 WNNFHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHRVAVIETIMIVYFLFWT 257
DB 190 WNFETLKMVILGLVPLLVVICYSGLIKTLRCRNEKKRHRVAVIETIMIVYFLFWA 249
QY 258 PYNIVILLNTQEFGLSNCSTESOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTYQEFFGLNCSNRLDQAMQVETLGMTHCCVNPPIIYAFVGEKERNYLL 309
QY 318 VFFRKHITRKCKOCVPYRETVDGVTSTNTPTSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQKEAPERANSVYTRSTGEQEISVGL 352

RESULT 8
Q18770 PRELIMINARY; PRT; 352 AA.
ID Q18770 PRELIMINARY; PRT; 352 AA.
AC Q18770;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MACCR5-140A;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.4;
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011538; AAB65738.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;

Query Match
Best Local Similarity 72.0%; Score 1368; DB 6; Length 352;
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVKQIGAOQLPPLYSLVFIFGVGNMVLVLLINCKKLCITDIYL 81
DB 10 YDIDYTSEPCQKINVKQIAARLPPLYSLVFIFGVGNMVLVLLINCKRLKSTDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHGYFGGIFFIILLTIDRYLA 141
DB 70 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITWVAVFASVPGIIFTKCKEDSVYVCGPYPRG----RG 197
DB 130 IVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHFPSYQYQF 189
QY 198 WNNFHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHRVAVIETIMIVYFLFWT 257
DB 190 WNFETLKMVILGLVPLLVVICYSGLIKTLRCRNEKKRHRVAVIETIMIVYFLFWA 249
QY 258 PYNIVILLNTQEFGLSNCSTESOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTYQEFFGLNCSNRLDQAMQVETLGMTHCCVNPPIIYAFVGEKERNYLL 309

Query Match
Best Local Similarity 72.2%; Score 1371; DB 6; Length 352;
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

QY 24 FDYDGA--PCHKFDVKQIGAOQLPPLYSLVFIFGVGNMVLVLLINCKKLCITDIYL 81
DB 10 YDIDYGASEPCQKTDVQKGAHLLPPLYSIVLFGVGNMVLVLLINCKRPSMTDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHGYFGGIFFIILLTIDRYLA 141
DB 70 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
DB 130 IVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFPGQYQF 189
QY 198 WNNFHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHRVAVIETIMIVYFLFWT 257
DB 190 WNFETLKMVILGLVPLLVVICYSGLIKTLRCRNEKKRHRVAVIETIMIVYFLFWA 249
QY 258 PYNIVILLNTQEFGLSNCSTESOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTYQEFFGLNCSNRLDQAMQVETLGMTHCCVNPPIIYAFVGEKERNYLL 309

```



```

ID Q95ND1 PRELIMINARY; PRT; 352 AA;
AC Q95ND1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Mandrillus sphinx (Mandrill) (Papio sphinx).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Mandrillus.
OX NCBI_TaxID=9561;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177897; AAK43360.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40510 MW; 402D8543DD3AEDD CRC64;

Query Match 71.9%; Score 1366; DB 6; Length 352;
Best Local Similarity 76.1%; Pred. No. 1.1e-109;
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKQIGAOQLPPLYSLVIFGVGNMVLVILINCKLKCLTDIYL 81
DB 10 YDIDYTSPPCKQKINVKQIAHLLPPLKSLVIFGVGNMVLVILINCKLKCLTDIYL 69
QY 82 LNLATSDLLFLTLPLWAHSAANEWFGNACKLFTGLYHIGYFGGIFFIILLTDIYLA 141
DB 70 LNLATSDLLFLTLPLWAHSAANEWFGNACKLFTGLYHIGYFGGIFFIILLTDIYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG 197
DB 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG 189
QY 198 WNNFHTIMRNILGLVPLLMIVICYSGLIKTLRLCRNEKKRRHRAVRVIFTIMIVYFLFWT 257
DB 190 WKNFRTLVILGLVPLLMIVICYSGLIKTLRLCRNEKKRRHRAVRVIFTIMIVYFLFWA 249
QY 258 PYNIVLLNTQEPFGLNCSSTOLDQATQVTELTGTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTQEPFGLNCSSTOLDQATQVTELTGTHCCINPIIYAFVGEKFRNYLL 309
QY 318 VFERKHITKRCCKCPVFEYRETVDGVTSTNTPTSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQEVSAVL 352

RESULT 12
Q95NC0 PRELIMINARY; PRT; 352 AA.
AC Q95NC0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates moloch (silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
phylogeny."

```

```

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177899; AAK43382.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 71.9%; Score 1366; DB 6; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.1e-109;
Matches 260; Conservative 30; Mismatches 47; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKQIGAOQLPPLYSLVIFGVGNMVLVILINCKLKCLTDIYL 81
DB 10 YDIDYTSPPCKQKINVKQIAHLLPPLKSLVIFGVGNMVLVILINCKLKCLTDIYL 69
QY 82 LNLATSDLLFLTLPLWAHSAANEWFGNACKLFTGLYHIGYFGGIFFIILLTDIYLA 141
DB 70 LNLATSDLLFLTLPLWAHSAANEWFGNACKLFTGLYHIGYFGGIFFIILLTDIYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG 197
DB 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG 189
QY 198 WNNFHTIMRNILGLVPLLMIVICYSGLIKTLRLCRNEKKRRHRAVRVIFTIMIVYFLFWT 257
DB 190 WKNFRTLVILGLVPLLMIVICYSGLIKTLRLCRNEKKRRHRAVRVIFTIMIVYFLFWA 249
QY 258 PYNIVLLNTQEPFGLNCSSTOLDQATQVTELTGTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTQEPFGLNCSSTOLDQATQVTELTGTHCCINPIIYAFVGEKFRNYLL 309
QY 318 VFERKHITKRCCKCPVFEYRETVDGVTSTNTPTSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQEVSAVL 352

RESULT 13
Q9XS99 PRELIMINARY; PRT; 352 AA.
AC Q9XS99;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GORILLACCR;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR EMBL; AF105291; AAD20560.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 71.8%; Score 1365; DB 6; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.4e-109;
Matches 260; Conservative 31; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKQIGAOQLPPLYSLVIFGVGNMVLVILINCKLKCLTDIYL 81

```

Db 10 YDIDYTSPOCKTQVWQAARLLPLYSIFGVGNMLVILILNCKRLKSMTDIYL 69
QY 82 LNLAISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTGVTVTWLVAVFASVPGIIFTKCKEDSVVYCGPYFP---RG 197
Db 130 IVHAFALKARTVTGVTVTWLVAVFASVPGIIFTKCKEDSVVYCGPYFP---RG 189
QY 198 WNNFHTIMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVRVIITMIVYFLEWT 257
Db 190 WNNFHTIMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVRVIITMIVYFLEWT 249
QY 258 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFERKHTKRFCKOCQVYRETVDGVTSTNTPTSGEQEVSAGL 360
Db 310 VFERKHTKRFCKOCQVYRETVDGVTSTNTPTSGEQEVSAGL 352

RESULT 14

Q95NC5 PRELIMINARY; PRT; 352 AA.
AC Q95NC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177884; AAK43367.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40508 MW; P4F64B3AD5AF658A CRC64;

Query Match 71.8%; Score 1365; DB 6; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.4e-109;
Matches 260; Conservative 30; Mismatches 47; Indels 6; Gaps 2;
QY 24 FDYDY--GAPCHKFDVQIGAGLLPPLYSLVIFGVGNMLVILILNCKRLKSMTDIYL 81
Db 10 YDIDYTSPOCKTQVWQAARLLPLYSIFGVGNMLVILILNCKRLKSMTDIYL 69
QY 82 LNLAISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTGVTVTWLVAVFASVPGIIFTKCKEDSVVYCGPYFP---RG 197
Db 130 IVHAFALKARTVTGVTVTWLVAVFASVPGIIFTKCKEDSVVYCGPYFP---RG 189
QY 198 WNNFHTIMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVRVIITMIVYFLEWT 257
Db 190 WNNFHTIMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVRVIITMIVYFLEWT 249
QY 258 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309

Db 250 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFERKHTKRFCKOCQVYRETVDGVTSTNTPTSGEQEVSAGL 360
Db 310 VFERKHTKRFCKOCQVYRETVDGVTSTNTPTSGEQEVSAGL 352
RESULT 15
Q95ND2 PRELIMINARY; PRT; 352 AA.
AC Q95ND2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Mandrillus.
OX NCBI_TaxID=9568;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177876; AAK43359.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40543 MW; 4C0CF4A2B8E5EFAF CRC64;

Query Match 71.8%; Score 1364; DB 6; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.7e-109;
Matches 260; Conservative 32; Mismatches 45; Indels 6; Gaps 2;
QY 24 FDYDY--GAPCHKFDVQIGAGLLPPLYSLVIFGVGNMLVILILNCKRLKSMTDIYL 81
Db 10 YDIDYTSPOCKTQVWQAARLLPLYSIFGVGNMLVILILNCKRLKSMTDIYL 69
QY 82 LNLAISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTGVTVTWLVAVFASVPGIIFTKCKEDSVVYCGPYFP---RG 197
Db 130 IVHAFALKARTVTGVTVTWLVAVFASVPGIIFTKCKEDSVVYCGPYFP---RG 189
QY 198 WNNFHTIMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVRVIITMIVYFLEWT 257
Db 190 WNNFHTIMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVRVIITMIVYFLEWT 249
QY 258 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVILLNTQFEGFLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFERKHTKRFCKOCQVYRETVDGVTSTNTPTSGEQEVSAGL 360
Db 310 VFERKHTKRFCKOCQVYRETVDGVTSTNTPTSGEQEVSAGL 352
Search completed: May 19, 2003, 16:48:13
Job time : 56.4414 secs

